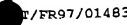
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[Translation of the claims as published along with the International application)

CLAIMS

- Fragment of nucleic acids specific mycchacteria 5 belonging to the M. tuberculosis complex, comprising a sequence of nucleotides selected from the sequence SEQ 2, the sequence SEQ No. IJ No. ID complementary sequences or the sequences of nucleic acids capable of hybridizing with one of the preceding 10 sequences under conditions of high stringency.
- Fragment of nucleic acids specific to /the 2. M. tuberculosis complex, comprising a sequence nucleotides selected from the sequence SEQ ID No. 1, its complementary sequence or the sequences of nucleic 15 acids capable of hybridizing with one of the preceding sequences under conditions of high stringency.
- Fragment of nucleic acids specific to members 3. of the M. tuberculosis complex which are different from BCG, comprising a sequence of nucleotides selected from 20 the sequence SEQ ID No. 2, its complementary sequence nucíeic acida capable ΟÍ sequences the hybridizing with one of the preceding sequences under conditions of high stringency.
- Cloning and/or /expression vector containing a 25 sequence of nucleic agics according to Claim 1.
 - Vector according to Claim 4, characterized in the plasmid pRegX3Bcl or PRegX3Mtl it is respectively deposited at the CNCM under the numbers I-1765 and I 1766.
 - or nucleotide probe Nucleotide characterized in that it hybridizes specifically with any one of the sequences according to Claim 1, the corresponding RNA sequences or the corresponding genes.
- according to Nucleotide probe 35 comprising 24 consecutive nucleotides selected from the sequences of nucleic acids according to Claim 1.

8. Nucleotide probe according to Claim 5, characterized in that it comprises the sequence SED ID No. 1 or its complementary strand.

characterized in that it comprises two successive sequences SEQ ID No. 1, followed by a sequence SEO ID No. 2.

10. Nucleotide probe for the detection of specific sequences of nucleic acids of members of the M. tuberculosis complex which are different from BCG, characterized in that it is a sequence corresponding to the region of the sequence SEQ ID No. 2 surrounding the GAG codon in the positions 40 to 42 or of its complementary strand.

15 11. Nucleotide probe according to Claim 10, characterized in that it is a sequence composed of 9 base pairs upstream and 9 base pairs downstream of the GAG codon in the specific positions 40 to 42 of the sequence SEQ ID No. 2.

20 12. Nucleotide probe according to Claim 10, characterized in that it is the sequence SEQ ID No. 2 or its complementary strand.

13. Nucleotice probe according to Claim 6, characterized in that it is labelled by dioxygonin.

Nucleotide primers for the amplification of a specific nucleotide sequence of mycobacteria belonging to the M. tuberculosis complex, comprising nucleotide sequences corresponding to the sequences adjacent to the senx3-regX3 intergenic region, in the regions 3' of senX3 and 5' of regX3.

Primers according to Claim 14, characterized in that they comprise 19 nucleotides.

16. Primers according to Claim 14, characterized in that they are the pair of primers 5'GCGCGAGAGCCCGAACTGC3' and 5'GCGCAGCAGAAACCTCAGC3' Seq.LD NO:5)

17. Use of a sequence according to Claim 1, for the

17. Use of a sequence according to Claim 1, for the production of diagnostic nucleotide probes or of

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nucleotide primers which can be used in an enzymatiq amplification method.

- Use of a probe according to any one of Claims 6 to 13 as an in vitro tool for detection or/for diagnosis of strains of mycobacteria belonging to the M. tuberculosis complex.
- Method of detection of strains of mycobacteria to the M. tuberculosis complex in belonging biological sample, comprising the following steps:
- contacting the biological sample with a (1) pair of primers according to any one of glaims 6, 14 to 16 under conditions allowing hybridization of the said primers to the specific nucleic acids of strains of mycobacteria belonging to the M. Luberculosis complex;
 - amplification of the said nucleic acids; (ii)
- (iii) contacting a nucleotide probe according to any one of Claims 6 to 13 with the said biological sample under conditions allowing the formation of hybridization complexes between the said probe and the amplified sequences of nucliciacids;
- detection of the hybridization complexes (iv) formed.
- Method according to Claim 19, characterized in that step (111) is carried out with a nucleotide probe according to Claim 8/.
- Method of detection of the presence of members of the M. tukerculosis complex other than BCG in a biological sample according to Claim 19, characterized in that step /iii) is carried out with a nucleotide probe according to Claim 10.
- differential detection and of Methød οf diagnosis /of BCG and of other members in a biological M. tubercylosis complex charactcrized in that a detection method according to Claim 2/ is carried out and in a search is made among amplified nucleic acids capable οf hybridization complexes those are found which are

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likewise capable of forming hybridization complexes with a nucleotide probe according to Claim 13:

- Method according to Claim 21 or Claim 27 for differentiating an infection by BCG from an infection by a virulent mycobacterium of the M. tuberculosis complex in an immunodeficient subject.
- Method according to Claim 23, characterized in that the immunodeficient subject is a subject infected with HIV.
- 25. Method for the identification of groups of 10 mycobacteria belonging to the M. Kuberculosis complex, Characterized in that:
- the DNA of the said strains previously extracted with a pair of primers according to any one of Claims 6, 14 to 161 contacted under conditions 15 allowing a specific hydridization of the primers with one of the sequences lacdording to Claim 1 and the obtainment of amplification products, and
- the length of the amplification products obtained is measured. 20
 - Method according to Claim 25, characterized in that the pair of primers according to Claim 16 is used.
 - Wit for the in vitro identification of strains 27. of mycobacteria belonging to the M. tuberculosis complex in a biological sample comprising:
 - a pair of primers according to any one of Claims 6, 14 to 16;

the reagents necessary to allow amplification of the sequences of nucleic acids.